**PRESERVE ROW LEVEL QUERY 2 OUTPUT LIST**

84 files returned by the second row level query are listed and described below:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Directory** | **File** | **Description** | **Fields** (derived fields defined, PCORnet fields listed) |
| 1 | output\_agg | preserve\_rl\_v02.log | Log file for query | N/A |
| 2 | output\_agg | attrition.sas7bdat | Attrition table for steps in computational phenotype for mild-to-moderate chronic kidney disease. Additionally includes total number of patients in demographic table before any criteria applied (change to first row level query). | * step: attrition step description * step\_num: attrition step number * count: count distinct patids |
| 3 | output\_agg | cond\_codeset\_cts.sas7bdat | Counts per codeset for condition table | * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * codeset: name of codeset * year: calendar year * n\_patids: count distinct patids * n\_rows: count rows |
| 4 | output\_agg | cond\_dx\_cts.sas7bdat | Counts per diagnosis code for condition table | * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * condition: field from condition table * condition\_type: field from condition table * year: calendar year * n\_patids: count distinct patids * n\_rows: count rows |
| 5 | output\_agg | dem\_birth\_year.sas7bdat | Counts per birth year | * birth\_calendar\_year: calendar year of birth * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * n\_patids: count distinct patids |
| 6 | output\_agg | dem\_cats.sas7bdat | Counts per demographic category | * sex: field from demographic table * race: field from demographic table * hispanic: field from demographic table * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * n\_patids: count distinct patids |
| 7 | output\_agg | dem\_ce\_age.sas7bdat | Counts per cohort entry age in years | * ce\_age\_years: cohort entry age in years * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * n\_patids: count distinct patids |
| 8 | output\_agg | dem\_ce\_yr.sas7bdat | Counts per cohort entry calendar year | * ce\_calendar\_year: calendar year of cohort entry * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * n\_patids: count distinct patids |
| 9 | output\_agg | diag\_codeset\_cts.sas7bdat | Counts per codeset in diagnosis table | * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * codeset: name of codeset * year: calendar year * n\_patids: count distinct patids * n\_rows: count rows |
| 10 | output\_agg | diag\_dx\_cts.sas7bdat | Counts per diagnosis code in diagnosis table | * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * dx: field from diagnosis table * dx\_type: field from diagnosis table * year: calendar year * n\_patids: count distinct patids * n\_rows: count rows |
| 11 | output\_agg | disp\_codeset\_cts.sas7bdat | Counts per codeset in dispensing table | * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * codeset: name of codeset * year: calendar year * n\_patids: count distinct patids * n\_rows: count rows |
| 12 | output\_agg | disp\_rx\_cts.sas7bdat | Counts per medication code in dispensing table | * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * ndc: field from dispensing table * year: calendar year * n\_patids: count distinct patids * n\_rows: count rows |
| 13 | output\_agg | enc\_ced\_fu\_attr\_cht.sas7bdat | Distribution of follow-up from cohort entry date to last in-person encounter for attrition table cohort (computational phenotype) | * n\_patids: count distinct patids * mean\_days\_ced\_fu: mean days in-person follow-up * sd\_days\_ced\_fu: standard deviation days in-person follow-up * median\_days\_ced\_fu: median days in-person follow-up * min\_days\_ced\_fu: min days in-person follow-up * max\_days\_ced\_fu: max days in-person follow-up |
| 14 | output\_agg | enc\_ced\_fu\_ckd\_dx.sas7bdat | Distribution of follow-up from cohort entry date to last in-person encounter for ckd stage 2/3 diagnosis cohort | * n\_patids: count distinct patids * mean\_days\_ced\_fu: mean days in-person follow-up * sd\_days\_ced\_fu: standard deviation days in-person follow-up * median\_days\_ced\_fu: median days in-person follow-up * min\_days\_ced\_fu: min days in-person follow-up * max\_days\_ced\_fu: max days in-person follow-up |
| 15 | output\_agg | enc\_ced\_fu\_high\_scr.sas7bdat | Distribution of follow-up from cohort entry date to last in-person encounter for high serum creatinine cohort | * n\_patids: count distinct patids * mean\_days\_ced\_fu: mean days in-person follow-up * sd\_days\_ced\_fu: standard deviation days in-person follow-up * median\_days\_ced\_fu: median days in-person follow-up * min\_days\_ced\_fu: min days in-person follow-up * max\_days\_ced\_fu: max days in-person follow-up |
| 16 | output\_agg | enc\_ip\_fu\_attr\_cht.sas7bdat | Distribution of follow-up from first to last in-person encounter for attrition table cohort (computational phenotype) | * n\_patids: count distinct patids * mean\_days\_ip\_fu: mean days in-person follow-up * sd\_days\_ip\_fu: standard deviation days in-person follow-up * median\_days\_ip\_fu: median days in-person follow-up * min\_days\_ip\_fu: min days in-person follow-up * max\_days\_ip\_fu: max days in-person follow-up |
| 17 | output\_agg | enc\_ip\_fu\_ckd\_dx.sas7bdat | Distribution of follow-up from first to last in-person encounter for ckd stage 2/3 diagnosis cohort | * n\_patids: count distinct patids * mean\_days\_ip\_fu: mean days in-person follow-up * sd\_days\_ip\_fu: standard deviation days in-person follow-up * median\_days\_ip\_fu: median days in-person follow-up * min\_days\_ip\_fu: min days in-person follow-up * max\_days\_ip\_fu: max days in-person follow-up |
| 18 | output\_agg | enc\_ip\_fu\_high\_scr.sas7bdat | Distribution of follow-up from first to last in-person encounter for high serum creatinine cohort | * n\_patids: count distinct patids * mean\_days\_ip\_fu: mean days in-person follow-up * sd\_days\_ip\_fu: standard deviation days in-person follow-up * median\_days\_ip\_fu: median days in-person follow-up * min\_days\_ip\_fu: min days in-person follow-up * max\_days\_ip\_fu: max days in-person follow-up |
| 19 | output\_agg | enc\_type\_cts.sas7bdat | Counts per encounter type in encounter table | * enc\_type: field from encounter table * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * year: calendar year * n\_patids: count distinct patids * n\_rows: count rows |
| 20 | output\_agg | lab\_codeset\_cts.sas7bdat | Counts per codeset in lab\_result\_cm table | * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * codeset: name of codeset * year: calendar year * n\_patids: count distinct patids * n\_rows: count rows |
| 21 | output\_agg | lab\_loinc\_cts.sas7bdat | Counts per loinc code in lab\_result\_cm table | * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * lab\_loinc: field from lab\_result\_cm table * year: calendar year * n\_patids: count distinct patids * n\_rows: count rows |
| 22 | output\_agg | lab\_vals1.sas7bdat | Distribution of qualitative lab results | * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * lab\_loinc: field from lab\_result\_cm table * result\_qual: field from lab\_result\_cm table * result\_snomed: field from lab\_result\_cm table * n\_patids: count distinct patids * n\_rows: count rows |
| 23 | output\_agg | lab\_vals2\_attr\_cht.sas7bdat | Distribution of numeric lab results for attrition table cohort (computational phenotype) | * n\_patids: count distinct patids * lab\_loinc: field from lab\_result\_cm table * result\_unit: field from lab\_result\_cm table * mean\_result\_num: mean result\_num (field from lab\_result\_cm table) * median\_result\_num: median result\_num * sd\_result\_num: standard deviation result\_num * min\_result\_num: minimum result\_num * max\_result\_num: maximum result\_num * n\_rows: count rows |
| 24 | output\_agg | lab\_vals2\_ckd\_dx.sas7bdat | Distribution of numeric lab results for ckd stage 2/3 diagnosis cohort | * n\_patids: count distinct patids * lab\_loinc: field from lab\_result\_cm table * result\_unit: field from lab\_result\_cm table * mean\_result\_num: mean result\_num (field from lab\_result\_cm table) * median\_result\_num: median result\_num * sd\_result\_num: standard deviation result\_num * min\_result\_num: minimum result\_num * max\_result\_num: maximum result\_num * n\_rows: count rows |
| 25 | output\_agg | lab\_vals2\_high\_scr.sas7bdat | Distribution of numeric lab results for high serum creatinine cohort | * n\_patids: count distinct patids * lab\_loinc: field from lab\_result\_cm table * result\_unit: field from lab\_result\_cm table * mean\_result\_num: mean result\_num (field from lab\_result\_cm table) * median\_result\_num: median result\_num * sd\_result\_num: standard deviation result\_num * min\_result\_num: minimum result\_num * max\_result\_num: maximum result\_num * n\_rows: count rows |
| 26 | output\_agg | lab\_vals3.sas7bdat | Distribution of norm\_range\_high and norm\_range\_low values in lab\_result\_cm table | * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * lab\_loinc: field from lab\_result\_cm table * result\_unit: field from lab\_result\_cm table * norm\_range\_high: field from lab\_result\_cm table * norm\_range\_low: field from lab\_result\_cm table * n\_patids: count distinct patids * n\_rows: count rows |
| 27 | output\_agg | lab\_vals4.sas7bdat | Distribution of raw qualitative lab results | * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * lab\_loinc: field from lab\_result\_cm table * concept\_name: description of lab\_loinc code * raw\_result: field from lab\_result\_cm table * result\_qual: field from lab\_result\_cm table * n\_patids: count distinct patids * n\_rows: count rows |
| 28 | output\_agg | lab\_vals5.sas7bdat | Distribution of raw\_lab\_name in lab\_result\_cm table | * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * lab\_loinc: field from lab\_result\_cm table * raw\_lab\_name: field from lab\_result\_cm table * n\_patids: count distinct patids * n\_rows: count rows |
| 29 | output\_agg | lab\_vals6.sas7bdat | Counts of missing result\_num | * lab\_loinc: field from lab\_result\_cm table * n\_rows: count rows |
| 30 | output\_agg | lab\_vals7.sas7bdat | Counts of missing norm\_range\_low | * lab\_loinc: field from lab\_result\_cm table * n\_rows: count rows |
| 31 | output\_agg | lab\_vals8.sas7bdat | Counts of missing norm\_range\_high | * lab\_loinc: field from lab\_result\_cm table * n\_rows: count rows |
| 32 | output\_agg | med\_codeset\_cts.sas7bdat | Counts per codeset in med\_admin table | * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * codeset: name of codeset * year: calendar year * n\_patids: count distinct patids * n\_rows: count rows |
| 33 | output\_agg | med\_rx\_cts.sas7bdat | Count per medication code in med\_admin table | * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * year: calendar year * medadmin\_code: field from med\_admin table * medadmin\_type: field from med\_admin table * n\_patids: count distinct patids * n\_rows: count rows |
| 34 | output\_agg | pres\_codeset\_cts.sas7bdat | Counts per codeset in prescribing table | * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * codeset: name of codeset * year: calendar year * n\_patids: count distinct patids * n\_rows: count rows |
| 35 | output\_agg | pres\_rx\_cts.sas7bdat | Counts per medication code in prescribing table | * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * rxnorm\_cui: field from prescribing table * year: calendar year * n\_patids: count distinct patids * n\_rows: count rows |
| 36 | output\_agg | proc\_codeset\_cts.sas7bdat | Counts per codeset in procedure table | * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * codeset: name of codeset * year: calendar year * n\_patids: count distinct patids * n\_rows: count rows |
| 37 | output\_agg | proc\_px\_cts.sas7bdat | Counts per procedure code in procedure table | * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * px: field from procedure table * px\_type: field from procedure table * year: calendar year * n\_patids: count distinct patids * n\_rows: count rows |
| 38 | output\_agg | prov\_neph.sas7bdat | Counts of nephrology visits | * enc\_type: field from encounter table * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * year: calendar year * n\_patids: count distinct patids * n\_rows: count rows |
| 39 | output\_agg | total\_cts.sas7bdat | Total patient counts for attrition table cohort, high serum creatinine cohort, and ckd diagnosis cohort. | * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * n\_patids: count distinct patids |
| 40 | output\_agg | unmap\_neph.sas7bdat | Counts of potentially unmapped or mis-mapped nephrology raw\_provider\_specialty\_primary | * provider\_specialty\_primary: field from provider table * raw\_provider\_specialty\_primary: field from provider table * n\_providers: count distinct providerids |
| 41 | output\_agg | unmap\_prot.sas7bdat | Counts of potentially unmapped or mis-mapped protein raw\_lab\_name | * lab\_loinc: field from lab\_result\_cm table * raw\_lab\_name: field from lab\_result\_cm table * specimen\_source: field from lab\_result\_cm table * n\_patids: count distinct patids * n\_rows: count rows |
| 42 | output\_agg | unmap\_scr1.sas7bdat | Counts of potentially unmapped or mis-mapped creatinine raw\_lab\_name | * lab\_loinc: field from lab\_result\_cm table * raw\_lab\_name: field from lab\_result\_cm table * specimen\_source: field from lab\_result\_cm table * n\_patids: count distinct patids * n\_rows: count rows |
| 43 | output\_agg | unmap\_scr2.sas7bdat | Counts of potentially unmapped or mis-mapped creatinine raw\_lab\_code | * lab\_loinc: field from lab\_result\_cm table * raw\_lab\_code: field from lab\_result\_cm table * n\_patids: count distinct patids * n\_rows: count rows |
| 44 | output\_agg | vital\_dia\_bp\_cts.sas7bdat | Counts of diastolic blood pressure measurements | * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * year: calendar year * n\_patids: count distinct patids * n\_rows: count rows |
| 45 | output\_agg | vital\_dia\_bp\_vals\_attr\_cht.sas7bdat | Distribution of diastolic blood pressure measurements for attrition table cohort (computational phenotype) | * n\_patids: count distinct patids * age\_years: age in years * mean\_dia\_bp: mean diastolic blood pressure * sd\_dia\_bp: standard deviation diastolic blood pressure * median\_dia\_bp: median diastolic blood pressure * min\_dia\_bp: minimum diastolic blood pressure * max\_dia\_bp: maximum diastolic blood pressure |
| 46 | output\_agg | vital\_dia\_bp\_ckd\_dx.sas7bdat | Distribution of diastolic blood pressure measurements for ckd stage 2/3 diagnosis cohort | * n\_patids: count distinct patids * age\_years: age in years * mean\_dia\_bp: mean diastolic blood pressure * sd\_dia\_bp: standard deviation diastolic blood pressure * median\_dia\_bp: median diastolic blood pressure * min\_dia\_bp: minimum diastolic blood pressure * max\_dia\_bp: maximum diastolic blood pressure |
| 47 | output\_agg | vital\_dia\_bp\_vals\_high\_scr.sas7bdat | Distribution of diastolic blood pressure measurements for high serum creatinine cohort | * n\_patids: count distinct patids * age\_years: age in years * mean\_dia\_bp: mean diastolic blood pressure * sd\_dia\_bp: standard deviation diastolic blood pressure * median\_dia\_bp: median diastolic blood pressure * min\_dia\_bp: minimum diastolic blood pressure * max\_dia\_bp: maximum diastolic blood pressure |
| 48 | output\_agg | vital\_ht\_cts.sas7bdat | Counts of height measurements | * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * year: calendar year * n\_patids: count distinct patids * n\_rows: count rows |
| 49 | output\_agg | vital\_ht\_vals\_attr\_cht.sas7bdat | Distribution of height measurements for attrition table cohort (computational phenotype) | * n\_patids: count distinct patids * age\_years: age in years * mean\_height\_in: mean height (inches) * sd\_height\_in: standard deviation height (inches) * median\_height\_in: median height (inches) * min\_height\_in: minimum height (inches) * max\_height\_in: maximum height (inches) |
| 50 | output\_agg | vital\_ht\_vals\_ckd\_dx.sas7bdat | Distribution of height measurements for ckd stage 2/3 diagnosis cohort | * n\_patids: count distinct patids * age\_years: age in years * mean\_height\_in: mean height (inches) * sd\_height\_in: standard deviation height (inches) * median\_height\_in: median height (inches) * min\_height\_in: minimum height (inches) * max\_height\_in: maximum height (inches) |
| 51 | output\_agg | vital\_ht\_vals\_high\_scr.sas7bdat | Distribution of height measurements for high serum creatinine cohort | * n\_patids: count distinct patids * age\_years: age in years * mean\_height\_in: mean height (inches) * sd\_height\_in: standard deviation height (inches) * median\_height\_in: median height (inches) * min\_height\_in: minimum height (inches) * max\_height\_in: maximum height (inches) |
| 52 | output\_agg | vital\_sys\_bp\_cts.sas7bdat | Counts of systolic blood pressure measurement | * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * year: calendar year * n\_patids: count distinct patids * n\_rows: count rows |
| 53 | output\_agg | vital\_sys\_bp\_vals\_attr\_cht.sas7bdat | Distribution of systolic blood pressure measurements for attrition table cohort (computational phenotype) | * n\_patids: count distinct patids * age\_years: age in years * mean\_sys\_bp: mean systolic blood pressure * sd\_sys\_bp: standard deviation systolic blood pressure * median\_sys\_bp: median systolic blood pressure * min\_sys\_bp: minimum systolic blood pressure * max\_sys\_bp: maximum systolic blood pressure |
| 54 | output\_agg | vital\_sys\_bp\_vals\_ckd\_dx.sas7bdat | Distribution of systolic blood pressure measurements for ckd stage 2/3 diagnosis cohort | * n\_patids: count distinct patids * age\_years: age in years * mean\_sys\_bp: mean systolic blood pressure * sd\_sys\_bp: standard deviation systolic blood pressure * median\_sys\_bp: median systolic blood pressure * min\_sys\_bp: minimum systolic blood pressure * max\_sys\_bp: maximum systolic blood pressure |
| 55 | output\_agg | vital\_sys\_bp\_vals\_high\_scr.sas7bdat | Distribution of systolic blood pressure measurements for high serum creatinine cohort | * n\_patids: count distinct patids * age\_years: age in years * mean\_sys\_bp: mean systolic blood pressure * sd\_sys\_bp: standard deviation systolic blood pressure * median\_sys\_bp: median systolic blood pressure * min\_sys\_bp: minimum systolic blood pressure * max\_sys\_bp: maximum systolic blood pressure |
| 56 | output\_agg | vital\_wt\_cts.sas7bdat | Counts of weight measurements | * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort * year: calendar year * n\_patids: count distinct patids * n\_rows: count rows |
| 57 | output\_agg | vital\_wt\_vals\_attr\_cht.sas7bdat | Distribution of weight measurements for attrition table cohort (computational phenotype) | * n\_patids: count distinct patids * age\_years: age in years * mean\_weight\_lb: mean weight (lbs) * sd\_weight\_lb: standard deviation weight (lbs) * median\_weight\_lb: median weight (lbs) * min\_weight\_lb: minimum weight (lbs) * max\_weight\_lb: maximum weight (lbs) |
| 58 | output\_agg | vital\_wt\_vals\_ckd\_dx.sas7bdat | Distribution of weight measurements for ckd stage 2/3 diagnosis cohort | * n\_patids: count distinct patids * age\_years: age in years * mean\_weight\_lb: mean weight (lbs) * sd\_weight\_lb: standard deviation weight (lbs) * median\_weight\_lb: median weight (lbs) * min\_weight\_lb: minimum weight (lbs) * max\_weight\_lb: maximum weight (lbs) |
| 59 | output\_agg | vital\_wt\_vals\_high\_scr.sas7bdat | Distribution of weight measurements for high serum creatinine cohort | * n\_patids: count distinct patids * age\_years: age in years * mean\_weight\_lb: mean weight (lbs) * sd\_weight\_lb: standard deviation weight (lbs) * median\_weight\_lb: median weight (lbs) * min\_weight\_lb: minimum weight (lbs) * max\_weight\_lb: maximum weight (lbs) |
| 60 | output\_row | attr\_cht.sas7bdat | Information about attrition cohort membership and entry | * patid * ce\_date: date of cohort entry |
| 61 | output\_row | attr\_chtstep7.sas7bdat | Information about attrition cohort membership and entry at step 7 of the attrition | * patid * ce\_date: date of cohort entry |
| 62 | output\_row | condition.sas7bdat | PCORnet table, restricted to “broad CKD cohort” and specified fields | conditionid, patid, encounterid, report\_date, resolve\_date, onset\_date, condition\_status, condition, condition\_type, condition\_source, raw\_condition, raw\_condition\_type |
| 63 | output\_row | broad\_ckd\_cht\_info.sas7bdat | Information about broad CKD cohort membership and entry | * patid * ce\_date: date of cohort entry * ce\_year: year of cohort entry * ce\_age\_years: age in years at cohort entry * attr\_cht: member of attrition table cohort (computational phenotype) * high\_scr: member of high serum creatinine cohort * ckd\_dx: member of ckd diagnosis cohort |
| 64 | output\_row | broad\_ckd\_cht\_info.sas7bndx | Index file for broad\_ckd\_cht\_info dataset above |  |
| 65 | output\_row | death.sas7bdat | PCORnet table, restricted to “broad CKD cohort” and specified fields | patid, death\_date, death\_date\_impute, death\_source, death\_match\_confidence |
| 66 | output\_row | death\_cause.sas7bdat | PCORnet table, restricted to “broad CKD cohort” and specified fields | patid, death\_cause, death\_cause\_code, death\_cause\_type, death\_cause\_source, death\_cause\_confidence |
| 67 | output\_row | demographic.sas7bdat | PCORnet table, restricted to “broad CKD cohort” and specified fields | patid, birth\_date, birth\_time, sex, hispanic, race |
| 68 | output\_row | diagnosis.sas7bdat | PCORnet table, restricted to “broad CKD cohort” and specified fields | diagnosisid, patid, encounterid, enc\_type, admit\_date, providerid, dx, dx\_type, dx\_date, dx\_source, dx\_origin, pdx, dx\_poa, raw\_dx |
| 69 | output\_row | dispensing.sas7bdat | PCORnet table, restricted to “broad CKD cohort” and specified fields | dispensingid, patid, prescribingid, dispense\_date, ndc, dispense\_source, dispense\_sup, dispense\_amt, dispense\_dose\_disp, dispense\_dose\_disp\_unit, dispense\_route, raw\_ndc |
| 70 | output\_row | encounter.sas7bdat | PCORnet table, restricted to “broad CKD cohort” and specified fields | encounterid, patid, admit\_date, admit\_time, discharge\_date, discharge\_time, providerid, enc\_type, facilityid, discharge\_disposition, discharge\_status, drg, drg\_type, admitting\_source, payer\_type\_primary, payer\_type\_secondary, facility\_type, raw\_facility\_type, facility\_location |
| 71 | output\_row | enrollment.sas7bdat | PCORnet table, restricted to “broad CKD cohort” and specified fields | patid, enr\_start\_date, enr\_end\_date, enr\_basis |
| 72 | output\_row | lab\_result\_cm.sas7bdat | PCORnet table, restricted to “broad CKD cohort” and specified fields | lab\_result\_cm\_id, patid, encounterid, specimen\_source, lab\_loinc, lab\_result\_source, lab\_loinc\_source, priority, result\_loc, lab\_px, lab\_px\_type, lab\_order\_date, specimen\_date, specimen\_time, result\_date, result\_time, result\_qual, result\_snomed, result\_num, result\_modifier, result\_unit, norm\_range\_low, norm\_modifier\_low, norm\_range\_high, norm\_modifier\_high, abn\_ind, raw\_lab\_code, raw\_result, raw\_unit, raw\_lab\_name |
| 73 | output\_row | med\_admin.sas7bdat | PCORnet table, restricted to “broad CKD cohort” and specified fields | medadminid, patid, encounterid, prescribingid, medadmin\_providerid, medadmin\_start\_date, medadmin\_start\_time, medadmin\_stop\_date, medadmin\_stop\_time, medadmin\_type, medadmin\_code, medadmin\_dose\_admin, medadmin\_dose\_admin\_unit, medadmin\_route, medadmin\_source, raw\_medadmin\_code |
| 74 | output\_row | obs\_clin.sas7bdat | PCORnet table, restricted to “broad CKD cohort”, birth weight, and specified fields | obsclinid, patid, encounterid, obsclin\_providerid, obsclin\_start\_date, obsclin\_start\_time, obsclin\_stop\_date, obsclin\_stop\_time, obsclin\_type, obsclin\_code, obsclin\_result\_qual, obsclin\_result\_snomed, obsclin\_result\_num, obsclin\_result\_modifier, obsclin\_result\_unit, obsclin\_source, obsclin\_abn\_ind, raw\_obsclin\_code, raw\_obsclin\_type |
| 75 | output\_row | obs\_gen\_gest\_age.sas7bdat | PCORnet table, restricted to “broad CKD cohort”, gestational age, and specified fields | obsgenid, patid, encounterid, obsgen\_providerid, obsgen\_start\_date, obsgen\_start\_time, obsgen\_stop\_date, obsgen\_stop\_time, obsgen\_type, obsgen\_code, obsgen\_result\_qual, obsgen\_result\_text, obsgen\_result\_num, obsgen\_result\_unit, obsgen\_table\_modified, obsgen\_id\_modified, obsgen\_source, obsgen\_abn\_ind, raw\_obsgen\_code, raw\_obsgen\_type, raw\_obsgen\_result, raw\_obsgen\_unit |
| 76 | output\_row | prescribing.sas7bdat | PCORnet table, restricted to “broad CKD cohort” and specified fields | prescribingid, patid, encounterid, rx\_providerid, rx\_order\_date, rx\_order\_time, rx\_start\_date, rx\_end\_date, rx\_dose\_ordered, rx\_dose\_ordered\_unit, rx\_quantity, rx\_dose\_form, rx\_refills, rx\_days\_supply, rx\_frequency, rx\_prn\_flag, rx\_route, rx\_basis, rxnorm\_cui, rx\_source, rx\_dispense\_as\_written, raw\_rxnorm\_cui |
| 77 | output\_row | procedures.sas7bdat | PCORnet table, restricted to “broad CKD cohort” and specified fields | proceduresid, patid, encounterid, enc\_type, admit\_date, providerid, px\_date, px, px\_type, px\_source, ppx, raw\_px, raw\_px\_type |
| 78 | output\_row | provider.sas7bdat | PCORnet table, restricted to “broad CKD cohort” and specified fields | * providerid, provider\_specialty\_primary, raw\_provider\_specialty\_primary |
| 79 | output\_row | row\_counts.sas7bdat | Counts of PCORnet tables extracted | * cdm\_table: PCORnet table * n\_patids: count patients * n\_rows: count rows |
| 80 | output\_row | vital.sas7bdat | PCORnet table, restricted to “broad CKD cohort” and specified fields | * vitalid, patid, encounterid, measure\_date, measure\_time, vital\_source, ht, wt, diastolic, systolic, original\_bmi, bp\_position, smoking, tobacco, tobacco\_type, raw\_diastolic, raw\_systolic, raw\_bp\_position |
| 81 | output\_geo | geo\_counts.sas7bdat | Counts of geographic-related PCORnet tables extracted | * cdm\_table: PCORnet table * n\_patids: count patients * n\_rows: count rows |
| 82 | output\_geo | lds\_address\_history\_zip5.sas7bdat | PCORnet table, restricted to “broad CKD cohort” and specified fields | addressid, patid, address\_use, address\_type, address\_preferred, address\_city, address\_state, address\_zip5, address\_period\_start, address\_period\_end |
| 83 | output\_geo | lds\_address\_history\_zip9.sas7bdat | PCORnet table, restricted to “broad CKD cohort” and specified fields | addressid, patid, address\_use, address\_type, address\_preferred, address\_city, address\_state, address\_zip5, address\_zip9, address\_period\_start, address\_period\_end |
| 84 | output\_geo | obs\_gen\_geo.sas7bdat | PCORnet table, restricted to “broad CKD cohort”, census tract or census block group, and specified fields | obsgenid, patid, encounterid, obsgen\_providerid, obsgen\_start\_date, obsgen\_start\_time, obsgen\_stop\_date, obsgen\_stop\_time, obsgen\_type, obsgen\_code, obsgen\_result\_qual, obsgen\_result\_text, obsgen\_result\_num, obsgen\_result\_unit, obsgen\_table\_modified, obsgen\_id\_modified, obsgen\_source, obsgen\_abn\_ind, raw\_obsgen\_code, raw\_obsgen\_type, raw\_obsgen\_result, raw\_obsgen\_unit |